# RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.**

Application Serial Number: _O9/487,841A_
Source: _1 FW16_
Date Processed by STIC: _2/11/05_

# *ENTERED*

RAW SEQUENCE LISTING                          DATE: 02/11/2005
PATENT APPLICATION:  US/09/487,841A          TIME: 18:44:57

Input Set : **A:\PTO.AMC.txt**
Output Set: **N:\CRF4\02112005\I487841A.raw**

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 4 <110> APPLICANT: Gravel, Roy A,
 5         Rozen, Rima
 6         Leclerc, Daniel
 7         Wilson, Aaron
 8         Rosenblatt, David
10 <120> TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE REDUCTASE:
11         CLONING, AND METHODS FOR EVALUATING RISK OF NEURAL TUBE
12         DEFECTS, CARDIOVASCULAR DISEASE, CANCER, AND DOWN'S SYNDROME
15 <130> FILE REFERENCE: 50004/003004
17 <140> CURRENT APPLICATION NUMBER: 09/487,841A
18 <141> CURRENT FILING DATE: 2000-01-19
20 <150> PRIOR APPLICATION NUMBER: 09/371,347
21 <151> PRIOR FILING DATE: 1999-08-10
23 <150> PRIOR APPLICATION NUMBER: 09/232,028
24 <151> PRIOR FILING DATE: 1999-01-15
26 <150> PRIOR APPLICATION NUMBER: 60/071,622
27 <151> PRIOR FILING DATE: 1998-01-16
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34 <211> LENGTH: 2097
35 <212> TYPE: DNA
36 <213> ORGANISM: Homo sapiens
38 <400> SEQUENCE: 1
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41 tccgataagt atgacctaaa aaccgaaaca gctcctcttg ttgttgtggt ttctaccacg 180
42 ggcaccggag acccacccga cacagcccgc aagtttgtta aggaaataca gaaccaaaca 240
43 ctgccggttg atttctttgc tcacctgcgg tatgggttac tgggtctcgg tgattcagaa 300
44 tacacctact tttgcaatgg ggggaagata attgataaac gacttcaaga gcttggagcc 360
45 cggcatttct atgacactgg acatgcagat gactgtgtag gtttagaact tgtggttgag 420
46 ccgtggattg ctggactctg gccagccctc agaaagcatt ttaggtcaag cagaggacaa 480
47 gaggagataa gtggcgcact cccggtggca tcacctgcat ccttgaggac agaccttgtg 540
48 aagtcagagc tgctacacat tgaatctcaa gtcgagcttc tgagattcga tgattcagga 600
49 agaaaggatt ctgaggtttt gaagcaaaat gcagtgaaca gcaaccaatc caatgttgta 660
50 attgaagact ttgagtcctc acttacccgt tcggtacccc cactctcaca agcctctctg 720
51 aatattcctg gtttaccccc agaatattta caggtacatc tgcaggagtc tcttggccag 780
52 gaggaaagcc aagtatctgt gacttcagca gatccagttt ttcaagtgcc aatttcaaag 840
53 gcagttcaac ttactacgaa tgatgccata aaaaccactc tgctggtaga attggacatt 900
54 tcaaatacag acttttccta tcagcctgga gatgccttca gcgtgatctg ccctaacagt 960
55 gattctgagg tacaaagcct actccaaaga ctgcagcttg aagataaaag agagcactgc 1020
56 gtccttttga aaataaaggc agacacaaag aagaaaggag ctaccttacc ccagcatata 1080
57 cctgcgggat gttctctcca gttcattttt acctggtgtc ttgaaatccg agcaattcct 1140
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58 aaaaaggcat ttttgcgagc ccttgtggac tataccagtg acagtgctga aaagcgcagg 1200
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61 ctgctcgaac atcttcctaa acttcaaccc agaccatatt cgtgtgcaag ctcaagttta 1380
62 tttcacccag gaaagctcca ttttgtcttc aacattgtgg aatttctgtc tactgccaca 1440
63 acagaggttc tgcggaaggg agtatgtaca ggctggctgg ccttgttggt tgcttcagtt 1500
64 cttcagccaa acatacatgc atcccatgaa gacagcggga aagccctggc tcctaagata 1560
65 tccatctctc ctcgaacaac aaattctttc cacttaccag atgacccctc aatccccatc 1620
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67 aaactccaag aacaacaccc agatggaaat tttggagcaa tgtggttgtt ttttggctgc 1740
68 aggcataagg atagggatta tctattcaga aaagagctca gacatttcct taagcatggg 1800
69 atcttaactc atctaaaggt ttccttctca agagatgctc ctgttgggga ggaggaagcc 1860
70 ccagcaaagt atgtacaaga caacatccag cttcatggcc agcaggtggc gagaatcctc 1920
71 ctccaggaga acggccatat ttatgtgtgt ggagatgcaa agaatatggc caaggatgta 1980
72 catgatgccc ttgtgcaaat aataagcaaa gaggttggag ttgaaaaact agaagcaatg 2040
73 aaaaccctgg ccactttaaa agaagaaaaa cgctaccttc aggatatttg gtcataa    2097
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76 <211> LENGTH: 698
77 <212> TYPE: PRT
78 <213> ORGANISM: Homo sapiens
80 <400> SEQUENCE: 2
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83 Ala Ile Ala Glu Glu Met Cys Glu Gln Ala Val Val His Gly Phe Ser
84             20                  25                  30
85 Ala Asp Leu His Cys Ile Ser Glu Ser Asp Lys Tyr Asp Leu Lys Thr
86         35                  40                  45
87 Glu Thr Ala Pro Leu Val Val Val Ser Thr Thr Gly Thr Gly Asp
88     50                  55                  60
89 Pro Pro Asp Thr Ala Arg Lys Phe Val Lys Glu Ile Gln Asn Gln Thr
90 65                  70                  75                  80
91 Leu Pro Val Asp Phe Phe Ala His Leu Arg Tyr Gly Leu Leu Gly Leu
92                 85                  90                  95
93 Gly Asp Ser Glu Tyr Thr Tyr Phe Cys Asn Gly Gly Lys Ile Ile Asp
94             100                 105                 110
95 Lys Arg Leu Gln Glu Leu Gly Ala Arg His Phe Tyr Asp Thr Gly His
96         115                 120                 125
97 Ala Asp Asp Cys Val Gly Leu Glu Leu Val Val Glu Pro Trp Ile Ala
98     130                 135                 140
99 Gly Leu Trp Pro Ala Leu Arg Lys His Phe Arg Ser Ser Arg Gly Gln
100 145                 150                 155                 160
101 Glu Glu Ile Ser Gly Ala Leu Pro Val Ala Ser Pro Ala Ser Leu Arg
102                 165                 170                 175
103 Thr Asp Leu Val Lys Ser Glu Leu Leu His Ile Glu Ser Gln Val Glu
104             180                 185                 190
105 Leu Leu Arg Phe Asp Asp Ser Gly Arg Lys Asp Ser Glu Val Leu Lys
106         195                 200                 205
107 Gln Asn Ala Val Asn Ser Asn Gln Ser Asn Val Val Ile Glu Asp Phe
108     210                 215                 220
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109 Glu Ser Ser Leu Thr Arg Ser Val Pro Pro Leu Ser Gln Ala Ser Leu
110 225                 230             235                 240
111 Asn Ile Pro Gly Leu Pro Pro Glu Tyr Leu Gln Val His Leu Gln Glu
112             245             250                 255
113 Ser Leu Gly Gln Glu Glu Ser Gln Val Ser Val Thr Ser Ala Asp Pro
114             260             265             270
115 Val Phe Gln Val Pro Ile Ser Lys Ala Val Gln Leu Thr Thr Asn Asp
116         275             280             285
117 Ala Ile Lys Thr Thr Leu Leu Val Glu Leu Asp Ile Ser Asn Thr Asp
118     290             295             300
119 Phe Ser Tyr Gln Pro Gly Asp Ala Phe Ser Val Ile Cys Pro Asn Ser
120 305             310             315                 320
121 Asp Ser Glu Val Gln Ser Leu Leu Gln Arg Leu Gln Leu Glu Asp Lys
122             325             330             335
123 Arg Glu His Cys Val Leu Leu Lys Ile Lys Ala Asp Thr Lys Lys Lys
124             340             345             350
125 Gly Ala Thr Leu Pro Gln His Ile Pro Ala Gly Cys Ser Leu Gln Phe
126         355             360             365
127 Ile Phe Thr Trp Cys Leu Glu Ile Arg Ala Ile Pro Lys Lys Ala Phe
128     370             375             380
129 Leu Arg Ala Leu Val Asp Tyr Thr Ser Asp Ser Ala Glu Lys Arg Arg
130 385             390             395                 400
131 Leu Gln Glu Leu Cys Ser Lys Gln Gly Ala Ala Asp Tyr Ser Arg Phe
132             405             410             415
133 Val Arg Asp Ala Cys Ala Cys Leu Leu Asp Leu Leu Leu Ala Phe Pro
134             420             425             430
135 Ser Cys Gln Pro Pro Leu Ser Leu Leu Leu Glu His Leu Pro Lys Leu
136         435             440             445
137 Gln Pro Arg Pro Tyr Ser Cys Ala Ser Ser Ser Leu Phe His Pro Gly
138     450             455             460
139 Lys Leu His Phe Val Phe Asn Ile Val Glu Phe Leu Ser Thr Ala Thr
140 465             470             475                 480
141 Thr Glu Val Leu Arg Lys Gly Val Cys Thr Gly Trp Leu Ala Leu Leu
142             485             490             495
143 Val Ala Ser Val Leu Gln Pro Asn Ile His Ala Ser His Glu Asp Ser
144             500             505             510
145 Gly Lys Ala Leu Ala Pro Lys Ile Ser Ile Ser Pro Arg Thr Thr Asn
146         515             520             525
147 Ser Phe His Leu Pro Asp Asp Pro Ser Ile Pro Ile Ile Met Val Gly
148     530             535             540
149 Pro Gly Thr Gly Ile Ala Pro Phe Ile Gly Phe Leu Gln His Arg Glu
150 545             550             555                 560
151 Lys Leu Gln Glu Gln His Pro Asp Gly Asn Phe Gly Ala Met Trp Leu
152             565             570             575
153 Phe Phe Gly Cys Arg His Lys Asp Arg Asp Tyr Leu Phe Arg Lys Glu
154             580             585             590
155 Leu Arg His Phe Leu Lys His Gly Ile Leu Thr His Leu Lys Val Ser
156         595             600             605
157 Phe Ser Arg Asp Ala Pro Val Gly Glu Glu Glu Ala Pro Ala Lys Tyr
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158      610                    615                  620
159 Val Gln Asp Asn Ile Gln Leu His Gly Gln Gln Val Ala Arg Ile Leu
160 625                    630                  635                  640
161 Leu Gln Glu Asn Gly His Ile Tyr Val Cys Gly Asp Ala Lys Asn Met
162                   645                  650                  655
163 Ala Lys Asp Val His Asp Ala Leu Val Gln Ile Ile Ser Lys Glu Val
164             660                  665                  670
165 Gly Val Glu Lys Leu Glu Ala Met Lys Thr Leu Ala Thr Leu Lys Glu
166          675                  680                  685
167 Glu Lys Arg Tyr Leu Gln Asp Ile Trp Ser
168      690                    695
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174 <213> ORGANISM: Homo sapiens
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181 <212> TYPE: DNA
182 <213> ORGANISM: Homo sapiens
184 <400> SEQUENCE: 4
185 aatagataat ccctatcctt atgcc                               25
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188 <211> LENGTH: 23
189 <212> TYPE: DNA
190 <213> ORGANISM: Homo sapiens
192 <400> SEQUENCE: 5
193 ccctggctcc taagatatcc atc                                 23
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196 <211> LENGTH: 26
197 <212> TYPE: DNA
198 <213> ORGANISM: Homo sapiens
200 <400> SEQUENCE: 6
201 cgaacaacaa attctttcca cttacc                              26
203 <210> SEQ ID NO: 7
204 <211> LENGTH: 23
205 <212> TYPE: DNA
206 <213> ORGANISM: Homo sapiens
208 <400> SEQUENCE: 7
209 caaggttggt ggaagtcgcg ttg                                 23
211 <210> SEQ ID NO: 8
212 <211> LENGTH: 25
213 <212> TYPE: DNA
214 <213> ORGANISM: Homo sapiens
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228 <211> LENGTH: 24
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244 <211> LENGTH: 23
245 <212> TYPE: DNA
246 <213> ORGANISM: Homo sapiens
248 <400> SEQUENCE: 12
249 cttgcacacg aatatggtct ggg                                     23
251 <210> SEQ ID NO: 13
252 <211> LENGTH: 23
253 <212> TYPE: DNA
254 <213> ORGANISM: Homo sapiens
256 <400> SEQUENCE: 13
257 tggcatcacc tgcatccttg agg                                     23
259 <210> SEQ ID NO: 14
260 <211> LENGTH: 25
261 <212> TYPE: DNA
262 <213> ORGANISM: Homo sapiens
264 <400> SEQUENCE: 14
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267 <210> SEQ ID NO: 15
268 <211> LENGTH: 24
269 <212> TYPE: DNA
270 <213> ORGANISM: Homo sapiens
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275 <210> SEQ ID NO: 16
276 <211> LENGTH: 25
277 <212> TYPE: DNA
278 <213> ORGANISM: Homo sapiens
280 <400> SEQUENCE: 16
281 ctcgaaatta accctcacta aaggg                                   25
283 <210> SEQ ID NO: 17
284 <211> LENGTH: 23
285 <212> TYPE: DNA
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VERIFICATION SUMMARY                    DATE: 02/11/2005
PATENT APPLICATION:   US/09/487,841A       TIME: 18:44:58

Input Set : **A:\PTO.AMC.txt**
Output Set: **N:\CRF4\02112005\I487841A.raw**